

SEQUENCE LISTING

<110> Meyers, Rachel A.
MacBeth, Kyle J.

<120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
USES THEREFOR

<130> 10448-046002

<150> US 09/633,300

<151> 2000-08-08

<150> US 60/200,621

<151> 2000-04-28

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (628)...(1986)

<221> misc_feature

<222> (1)...(2948)

<223> n = A,T,C or G

<400> 1

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gtatttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact    180
gttaccact ttgcctcgtc ttcaccctgt ccaaaccacg gtctccaatt tgcccttcag    240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca    300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc    360
caaactccaa aaaaaaaccc gaattcagcc tggttaagtc caagctgaat tccgggtggg    420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattagggtc atgcccgat    480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc    540
gtgggtgcat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg    600
gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt    654
                                Met Gly Glu Asn Asp Pro Pro Ala Val
                                1                               5

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gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa    702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
  10                      15                      20                      25

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ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg    750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
          30                      35                      40

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tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att	798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile	
45 50 55	
gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc	846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys	
60 65 70	
tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata	894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile	
75 80 85	
gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac	942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	
90 95 100 105	
cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca	990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr	
110 115 120	
gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac	1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr	
125 130 135	
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca	1086
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt	1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc	1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1470

Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro
 270 275 280
 gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag 1518
 Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys
 285 290 295
 cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca 1566
 Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro
 300 305 310
 ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa 1614
 Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
 315 320 325
 gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc 1662
 Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
 330 335 340 345
 aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc 1710
 Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
 350 355 360
 cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc 1758
 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
 365 370 375
 atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg 1806
 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
 380 385 390
 gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg 1854
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
 395 400 405
 agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca 1902
 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
 410 415 420 425
 gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac 1950
 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
 430 435 440
 tgg atc cac gag cag atg gag aga gac cta aaa acc tgaaaaggaa 1996
 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
 445 450
 ggggacaagt agccaccta gttcctgagg tgatgaagac agcccgatcc tcccctggac 2056
 tcccgtgtag gaacctgcac acgagcagac acccttgagg ctctgagttc cggcaccagt 2116
 agcaggcccc aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt 2176
 gttttttgtt tttttgagat ggagtctcgc tctgttgccc aggetggagt gcagtggcga 2236
 aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc 2296
 cccagtagct gggaccacag gtgcccgcga ccacacccaa ctaatttttg tatttttagt 2356
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 gctgtctca gctcccaca gtgctgggat tacaggcatg ggccaccacg cctagcctca 2476
 cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg ggggcctttc 2536
 ccactgggtcc atctgggttt ctctccaggg gtcttgcaaa attcctgacg agataagcag 2596

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ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga 2656
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aaccaccct 2716
ttctacttcc aagacttatt ttcacatgtg gggagggttaa tctaggaatg actcgtttaa 2776
ggcctatttt catgatttct ttgtagcatt tgggtgcttga cgtattattg tcctttgatt 2836
ccaaataata tgttttccttc cctcatwraa maaaaaaaaa aaaaaaaarr rmrrssgcta 2896
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<210> 2
<211> 453
<212> PRT
<213> Homo sapiens

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Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
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Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
      35      40      45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
      50      55      60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
      65      70      75      80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
      85      90      95
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
      100      105      110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
      115      120      125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
      130      135      140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
      145      150      155      160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
      165      170      175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
      180      185      190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
      195      200      205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
      210      215      220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
      225      230      235      240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
      245      250      255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
      260      265      270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
      275      280      285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
      290      295      300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
      305      310      315      320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
      325      330      335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
      340      345      350

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<210> 3
<211> 1362
<212> DNA
<213> Homo sapiens
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<210> 4
<211> 260
<212> PRT
<213> Artificial Sequence
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<400> 4
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 1          5          10          15
Gln Val Ser Leu Gln Val Arg Ser Gly Gly Gly Ser Arg Lys His Phe

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20 25 30
 Cys Gly Gly Ser Leu Ile Ser Glu Asn Trp Val Leu Thr Ala Ala His
 35 40 45
 Cys Val Ser Gly Ala Ala Ser Ala Pro Ala Ser Ser Val Arg Val Ser
 50 55 60
 Leu Ser Arg Val Arg Leu Gly Glu His Asn Leu Ser Leu Thr Glu Gly
 65 70 75 80
 Thr Glu Gln Lys Phe Asp Val Lys Lys Thr Ile Ile Val His Pro Asn
 85 90 95
 Tyr Asn Pro Asp Thr Leu Asp Asn Gly Ala Tyr Asp Asn Asp Ile Ala
 100 105 110
 Leu Leu Lys Leu Lys Ser Pro Gly Val Thr Leu Gly Asp Thr Val Arg
 115 120 125
 Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp Leu Pro Val Gly Thr Thr
 130 135 140
 Cys Thr Val Ser Gly Trp Gly Arg Arg Pro Thr Lys Asn Leu Gly Leu
 145 150 155 160
 Ser Asp Thr Leu Gln Glu Val Val Val Pro Val Val Ser Arg Glu Thr
 165 170 175
 Cys Arg Ser Ala Tyr Glu Tyr Gly Gly Thr Asp Asp Lys Val Glu Phe
 180 185 190
 Val Thr Asp Asn Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala
 195 200 205
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Asn Arg
 210 215 220
 Asp Gly Arg Trp Glu Leu Val Gly Ile Val Ser Trp Gly Ser Tyr Gly
 225 230 235 240
 Cys Ala Arg Gly Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr
 245 250 255
 Leu Asp Trp Ile
 260

<210> 5
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

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 Arg Ile Val Gly Gly Ser Glu Ala Lys Ile Gly Ser Phe Pro Trp Gln
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 Val Ser Leu Gln Cys Gly Gly Ser Leu Ile Ser Pro Arg Trp Val Leu
 20 25 30
 Thr Ala Ala His Cys Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 35 40 45
 Gly Glu Glu Thr Glu Gly Gly Pro Arg Leu Asp Ser Pro Gly Gly Gln
 50 55 60
 Val Ile Lys Val Ser Lys Ile Ile Glu Val His Pro Asn Tyr Asn Asn
 65 70 75 80
 Asp Ile Ala Leu Leu Lys Leu Lys Glu Pro Val Thr Leu Ser Asp Ser
 85 90 95
 Asn Thr Val Arg Pro Ile Cys Leu Pro Ser Ser Asn Glu Ile Lys Thr
 100 105 110
 Ser Glu Gly Asn Thr Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125

Trp Gly Arg Thr Ser Glu Gly Pro Glu Glu Ser Gly Gly Gly Ser Leu
 130 135 140
 Pro Asp Val Leu Gln Glu Val Asn Val Pro Ile Val Ser Asn Glu Thr
 145 150 155 160
 Cys Arg Met Leu Cys Ala Gly Tyr Leu Glu Gly Gly Asn Thr Pro Gly
 165 170 175
 Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Val
 180 185 190
 Leu Val Gly Ile Val Ser Trp Gly Ser Ser Ser Leu Tyr Gly Cys Ala
 195 200 205
 Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr Leu Asp
 210 215 220
 Trp Ile
 225

<210> 6
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 6
 Ser Thr Cys Gly Gly Pro Asp Glu Phe Gln Cys Gly Ser Gly Arg Arg
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 Cys Ile Pro Arg Ser Trp Val Cys Asp Gly Asp Pro Asp Cys Glu Asp
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 Gly Ser Asp Glu Ser Leu Glu Asn Cys Ala Ala
 35 40

<210> 7
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 7
 Val Gly Gly Ser Ser Arg Cys Glu Gly Arg Val Glu Val Arg His Asp
 1 5 10 15
 Gly Ser Lys Trp Gly Thr Val Cys Asp Ser Ser Trp Ser Leu Arg Asp
 20 25 30
 Ala Asn Val Asp Pro Gln Ala Ser Lys Val Cys Arg Gln Leu Gly Cys
 35 40 45
 Gly Gly Ala Val Ser Leu Leu Gly Pro Tyr Phe Ser Glu Gly Gly Gly
 50 55 60
 Pro Ala Gly Gln Arg Glu Ile Trp Leu Asp Gly Val Asn Cys Ser Gly
 65 70 75 80
 Asn Glu Thr Ser Leu Ser Gln Cys Pro Val Arg Val Thr Pro Pro Gly
 85 90 95
 Leu Ser Arg Gln Cys Ser His Asp Gly Glu Asp Ala Gly Val Val Cys
 100 105 110
 Ser

<210> 8
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 8
 Arg Ile Val Gly Gly
 1 5

<210> 9
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> motif

<221> VARIANT
 <222> 2
 <223> Xaa = Asp or Glu

<221> VARIANT
 <222> 5
 <223> Xaa = Gly or Ser

<400> 9
 Gly Xaa Ser Gly Xaa
 1 5

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> motif

<221> VARIANT
 <222> 1
 <223> Xaa = Leu, Ile, Val, or Met

<221> VARIANT
 <222> 2
 <223> Xaa = Ser or Thr

<221> VARIANT
 <222> 4
 <223> Xaa = Ser, Thr, Ala, or Gly

<400> 10
 Xaa Xaa Ala Xaa His Cys
 1 5

<210> 11
 <211> 2951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (628) ... (1989)

<221> misc_feature
 <222> (1) ... (2951)
 <223> n = A,T,C or G

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 gtattttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact 180
 gttacccact ttgcctcgtc ttcaccctgt ccaaacaccg gtctccaatt tgcccttcag 240
 agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatattca 300
 ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc 360
 caaactccaa aaaaaaacccg gaattcagcc tggttaagtc caagctgaat tccgggtggg 420
 ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattagggtc atgcccgtat 480
 gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc 540
 gtgggtgcat ctacattttt gggactcggg aattatgagg tagaggtgga ggcggagccg 600
 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 654
 Met Gly Glu Asn Asp Pro Pro Ala Val
 1 5

gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 702
 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10 15 20 25

ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 750
 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
 30 35 40

tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 798
 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
 45 50 55

gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 846
 Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys
 60 65 70

tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata 894
 Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
 75 80 85

gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac 942
 Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 90 95 100 105

cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca 990
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr
 110 115 120

gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac 1038
 Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr
 125 130 135

gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca 1086

Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt	1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc	1326
Val Gly Gly Asn Met Ser Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1470
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro	
270 275 280	
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag	1518
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys	
285 290 295	
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca	1566
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro	
300 305 310	
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa	1614
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu	
315 320 325	
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc	1662
Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala	
330 335 340 345	
aca gag gat gga gca ggt gac gcc tcc cct gtc ctg aac cac gcg gcc	1710
Thr Glu Asp Gly Ala Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala	
350 355 360	
gtc cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt	1758
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly	

365	370	375	
ggc atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc			1806
Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly			
380	385	390	
gtg gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag			1854
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu			
395	400	405	
agg agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc			1902
Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys			
410	415	420	425
gca gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg			1950
Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu			
430	435	440	
gac tgg atc cac gag cag atg gag aga gac cta aaa acc tgaagaggaa			1999
Asp Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr			
445	450		
ggggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac			2059
tcccgtgtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt			2119
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agagacaggg tttcaccatg ttggccaggc tgctctcaaa cccctgacct caaatgatgt			2419
gctgcttca gctcccaca gtgctgggat tacaggcatg ggccaccacg cctagcctca			2479
cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg gcggcctttc			2539
ccactggtcc atctggtttt ctctccaggg gtcttgcaaa attcctgacg agataagcag			2599
ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga			2659
agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aaccaccct			2719
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ggcctatttt catgatttct ttgtagcatt tgggtcttga cgtattattg tcctttgatt			2839
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